

SEQUENCE LISTING

<110> Braun, Jonathan
Sutton, Christopher L.

<120> IBD-Associated Microbial Nucleic Acid
Molecules

<130> P-PM 4966

<150> US 09/303,120

<151> 1999-04-30

<150> US 09/820,576

<151> 2001-03-28

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 302

<212> DNA

<213> Unknown

<220>

<223> Microbial Organism from the human gut

<221> CDS

<222> (2)...(301)

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Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His
1 5 10 15

ttc aag agc aag gat gag ata ttg cgt gcc gtg atg gag gaa acc atc 97
Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
20 25 30

cat tac aac acc gcg atg atg cgc gct tca ctg gag gag gcg agc acg 145
His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
35 40 45

gtg cgc gaa cgc gtg ctg gcg ctg atc cgc tgc gag ttg cag tcg atc 193
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
50 55 60

atg ggc ggc agt ggc gag gcc atg gcg gtg ctg gtc tac gaa tgg cgc 241
Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
65 70 75 80

09966603-09966603

tat gag cag atc t	302
Tyr Glu Gln Ile	
100	

<220>
<223> Microbial organism from the human gut

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<211> 392
<212> DNA
<213> Unknown
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<221> CDS
<222> (2) ... (346)

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<400> 3
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  Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro
    1             5             10             15
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gcg gat cga gag tgg gtg ttt ttt cag ggc acg gtt tcc tac aag gta 97
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val
20 25 30

cga gtg gcc agc cgt ttg ctc atc aat gaa agc cgg gca ttg atg tcg 145
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser
35 40 45

gcg gca ttg gat ggt ttt ggc ata gtg ctc ggc ccg caa gac ttc ctg 193
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu
50 55 60

cga acg gcg ttg gcg agt ggc gag ttg gtg cgg gtg ttg ccg gag ttt 241
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe
65 70 75 80

gag gct ccg agt cgg tcg atg cat ttg gtc tac acc gca aac cgc cag 289
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln
85 90 95

cgt acc gcc aag ttg cgc tgc ttt gtc gag act gtg ctg gga cgt ttt 337
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe
100 105 110

ggt ccg gta tgaaggagca ccaccgtggc ggtcgccggg angcacctaa 386
Gly Pro Val
115

agatct 392

<210> 4
<211> 115
<212> PRT
<213> Unknown

<220>
<223> Microbial organism from the human gut

<400> 4
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20 25 30
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser
35 40 45
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu
50 55 60
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe
65 70 75 80
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln
85 90 95
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe

099660-099660

100 105 110
Gly Pro Val
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<210> 5
<211> 114
<212> PRT
<213> Unknown

<220>
<223> Microbial Organism from the human gut

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<222> (1)...(114)
<223> Xaa = Any Amino Acid

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Gln His Arg Arg Cys Gln Ile Thr Lys Ala Tyr His Glu Ala Arg Leu
35 40 45
Val Glu Gln Ser Arg Arg Gln Arg Thr Ala Leu Gln His Pro His Gln
50 55 60
Arg Leu Lys Leu Ser Arg Thr Pro Arg His Met Gln Asp Val Gly Cys
65 70 75 80
Val Ala Leu Thr Gly Gly Leu Gln Ala Ala Lys Asp Leu Ser His Gln
85 90 95
Ser Thr Lys Thr Arg Tyr Ser Pro Ala Gly Gly His Arg Asp Gly Pro
100 105 110
Xaa Val

<210> 6
<211> 190
<212> PRT
<213> Clostridium pasteurianum

<400> 6
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Ser Asn Asn Gly Tyr Asn Gly Ala Thr Met Asp Glu Ile Ala Ser Asn
20 25 30
Ala Gly Val Ala Lys Gly Thr Leu Tyr Tyr His Phe Lys Ser Lys Glu
35 40 45
Glu Ile Phe Lys Tyr Ile Ile Glu Glu Gly Val Asn Leu Met Lys Asn
50 55 60
Glu Ile Asp Glu Ala Thr Asp Lys Glu Lys Thr Ala Leu Glu Lys Leu
65 70 75 80
Lys Ala Val Cys Arg Val Gln Leu Asn Leu Ile Tyr Lys Asn Arg Asp

10996603-0924

				85					90					95			
Phe	Phe	Lys	Val	Ile	Ala	Ser	Gln	Leu	Trp	Gly	Lys	Glu	Leu	Arg	Gln		
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Leu	Glu	Leu	Arg	Asp	Ile	Met	Arg	Asn	Tyr	Val	Val	His	Ile	Glu	Glu		
		115					120					125					
Phe	Val	Lys	Asp	Ala	Met	Glu	Ala	Gly	Ser	Ile	Lys	Lys	Gly	Asn	Ser		
		130				135					140						
Leu	Phe	Val	Ala	Tyr	Ala	Phe	Leu	Gly	Thr	Leu	Cys	Ser	Val	Ser	Leu		
145					150					155					160		
Tyr	Glu	Val	Ile	Asn	Ala	Glu	Asn	Asp	Asn	Ile	Asn	Asn	Thr	Ile	Glu		
			165					170						175			
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<210> 7
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 <212> PRT
 <213> Mycobacterium tuberculosis

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		20						25				30					
Val	Arg	Asp	Ile	Ala	Asp	Gly	Ala	Gly	Ile	Leu	Ser	Gly	Ser	Leu	Tyr		
		35				40					45						
His	His	Phe	Ala	Ser	Lys	Glu	Glu	Met	Val	Asp	Glu	Leu	Leu	Arg	Gly		
	50				55					60							
Phe	Leu	Asp	Trp	Leu	Phe	Ala	Arg	Tyr	Arg	Asp	Ile	Val	Asp	Ser	Thr		
65				70				75						80			
Ala	Asn	Pro	Leu	Glu	Arg	Leu	Gln	Gly	Leu	Phe	Met	Ala	Ser	Phe	Glu		
			85					90					95				
Ala	Ile	Glu	His	His	His	Ala	Gln	Val	Val	Ile	Tyr	Gln	Asp	Glu	Ala		
		100						105				110					
Gln	Arg	Leu	Ala	Ser	Gln	Pro	Arg	Phe	Ser	Tyr	Ile	Glu	Asp	Arg	Asn		
		115				120						125					
Lys	Gln	Gln	Arg	Lys	Met	Trp	Val	Asp	Val	Leu	Asn	Gln	Gly	Ile	Glu		
	130				135					140							
Glu	Gly	Tyr	Phe	Arg	Pro	Asp	Leu	Asp	Val	Asp	Leu	Val	Tyr	Arg	Phe		
145				150				155						160			
Ile	Arg	Asp	Thr	Thr	Trp	Val	Ser	Val	Arg	Trp	Tyr	Arg	Pro	Gly	Gly		
			165					170					175				
Pro	Leu	Thr	Ala	Gln	Gln	Val	Gly	Gln	Gln	Tyr	Leu	Ala	Ile	Val	Leu		
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Gly	Gly	Ile	Thr	Lys	Glu	Gly	Val										
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<210> 8
 <211> 192
 <212> PRT
 <213> Auifex aeolicus

09656001

<400> 8
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 Lys Ile Leu Ser Ser Ala Leu Lys Leu Phe Ser Lys Lys Gly Phe Lys
 20 25 30
 Glu Thr Thr Ile Lys Asp Ile Ala Lys Glu Val Gly Ile Thr Glu Gly
 35 40 45
 Ala Ile Tyr Arg His Phe Thr Ser Lys Glu Glu Ile Ile Lys Ser Leu
 50 55 60
 Leu Glu Ser Ile Thr Lys Glu Leu Arg His Lys Leu Glu Val Ala Leu
 65 70 75 80
 Gln Arg Gly Glu Thr Asp Glu Glu Ile Leu Glu Ser Ile Val Asp Thr
 85 90 95
 Leu Ile Asp Tyr Ala Phe Ser Asn Pro Glu Ser Phe Arg Phe Leu Asn
 100 105 110
 Leu Tyr His Leu Leu Lys Glu Tyr Gly Glu Val Lys Asn Leu Pro Gly
 115 120 125
 Glu Leu Ile Leu Lys Phe Leu Asn Gly Leu Tyr Leu Lys Arg Lys Leu
 130 135 140
 Lys Thr Tyr Pro Glu Ile Ala Leu Ala Val Val Thr Gly Ser Val Glu
 145 150 155 160
 Arg Val Phe Ile Phe Lys Glu Arg Asn Phe Leu Asp Tyr Asp Glu Glu
 165 170 175
 Thr Ile Lys Lys Glu Leu Lys Lys Val Leu Lys Ser Ala Ile Leu Ala
 180 185 190

<210> 9
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 <212> DNA
 <213> Unknown

 <220>
 <223> Microbial Organism from the human gut

<400> 9
 ccgtgggcat ccagtccg 18

<210> 10
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 <212> DNA
 <213> Unknown

<220>
 <223> Microbial Organism from the human gut

<400> 10
 tctgtcata cacgtcacg 19